

CRF Errors Corrected by the STIC Systems Branch

Team 8

Serial Number: 08/785,455

CRF Processing Date: 2/21/99
 Edited by: MC
 Verified by: MC (STIC staff)

ENTERED

#2

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inserted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☒ Deleted ~~extra~~ invalid, headings used by an applicant, specifically:
"APPLICANT"
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file;
☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a Patent bug). Sequences corrected: _____
- ☒ Other: added (B) FILING DATE: leading under (vi) CURRENT APPLICATION DATA:

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/785,455

DATE: 02/21/97

TIME: 15:30:00

INPUT SET: S15668.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information

(i) APPLICANT

(A) NAME: Hodgson, John
(B) STREET: Great West Road
(C) CITY: Brentford
(D) STATE OR PROVINCE: Middlesex
(E) COUNTRY: United Kingdom
(F) POSTAL CODE: TW8 9EP

~~APPLICANT~~

(A) NAME: Hodgson, John
(B) STREET: Great West Road
(C) CITY: Brentford
(D) STATE OR PROVINCE: Middlesex
(E) COUNTRY: United Kingdom
(F) POSTAL CODE: TW8 9EP

(ii) TITLE OF THE INVENTION: Novel tRNA Synthetase

(iii) NUMBER OF SEQUENCES: 2

(iv) COMPUTER-READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(v) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1974 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING PATENT APPLICATION US/08/785,455

DATE: 02/21/97

TIME: 15:30:03

INPUT SET: S15668.raw

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47  ATGGCTAAAG AAACATTTTA TATAACAACC CCAATATACT ATCCTAGTGG GAATTTACAT      60
48  ATAGGACATG CATATTCTAC AGTGGCTGGA GATGTTATTG CAAGATATAA GAGAATGCAA     120
49  GGATATGATG TTCGTTATTT GACTGGAACG GATGAACACG GTCAAAAAAT TCAAGAAAAA     180
50  GCTCAAAAAG CTGGTAAGAC AGAAATTGAA TATTTGGATG AGATGATTGC TGGAAATTAAA     240
51  CAATTGTGGG CTAAGCTTGA AATTTCAAAT GATGATTTTA TCAGAACAAC TGAAGAACGT     300
52  CATAAACATG TCGTTGAGCA AGTGTTTGAA CGTTTATTAA AGCAAGGTGA TATCTATTTA     360
53  GGTGAATATG AAGGTTGGTA TTCTGTTCCG GATGAAACAT ACTATACAGA GTCACAATTA     420
54  GTAGACCCAC AATACGAAAA CGGTAAAAAT AATTGGTGGCA AAAGTCCAGA TTCCTGGACAC     480
55  GAAGTTGAAC TAGTTAAAGA AGAAAGTTAT TTCTTTAATA TTAGTAAATA TACAGACCGT     540
56  TTATTAGAGT TCTATGACCA AAATCCAGAT TTTATACAAC CACCATCAAG AAAAAATGAA     600
57  ATGATTAACA ACTTCATTAA ACCAGGACTT GCTGATTTAG CTGTTTCTCG TACATCATTT     660
58  AACTGGGGTG TCCATGTTCC GTCTAATCCA AAACATGTTG TTTATGTTTG GATTGATGCG     720
59  TTAGTTAACT ATATTTTCAGC ATTAGGCTAT TATCAGATG ATGAGTCACT ATTTAACAAA     780
60  TACTGGCCAG CAGATATTCA TTTAATGGCT AAGGAAATTG TGCGATTCCA CTCAATTATT     840
61  TGGCCATTTT TATTGATGGC ATTAGACTTA CCGTTACCTA AAAAAGTCTT TGCACATGGT     900
62  TGGATTTTGA TGAAAGATGG AAAAAAGAGT AAATCTAAAG GTAATGTTGT AGACCCTAAT     960
63  ATTTTAAATT ATCGCTATGG TTTAGATGCT ACACGTTATT ATCTAATGCG TGAATTACCA    1020
64  TTTGGTTCAG ATGGCGTATT TACACCTGAA GCATTTGTTG AGCGTACAAA TTTCGATCTA    1080
65  GCAAAATGACT TAGGTAACCT AGTAAACCGT ACGATTTCTA TGGTTAATAA GTACTTTGAT    1140
66  GGCGAATTAC CAGCGTATCA AGGTCCACTT CATGAATTAG ATGAAGAAAT GGAAGCTATG    1200
67  GCTTTAGAAA CAGTGAAGAG CTACACTGAA AGCATGGAAA GTTTGCAATT TTCTGTGGCA    1260
68  TTATCTACGG TATGGAAGTT TATAAGTAGA ACGAATAAGT ATATTGACGA AACAACGCCCT    1320
69  TGGGTATTAG CTAAGGACGA TAGCCAAAAA GATATGTTAG GCAATGTAAT GGCTCACTTA    1380
70  GTTGAAAATA TTCGTTATGC AGCTGTATTA TTACGTCCAT TCTTAACACA TGCGCCGAAA    1440
71  GAGATTTTTG AACAAATGAA CATAAACAAAT CCTCAATTTA TGGAAATTAG TAGTTTAGAG    1500
72  CAATATGGTG TGCTTACTGA GTCAATTATG GTTACTGGGC AACCTAAACC TATTTTCCCA    1560
73  AGATTGGATA GCGAAGCGGA AATTGCATAT ATCAAAGAAT CAATGCAACC GCCTGCTACT    1620
74  GAAGAGGAAA AAGAAGAGAT TCCTAGCAAA CCTCAAATTG ATATTAAAGA CTTTGATAAA    1680
75  GTTGAAATTA AGGCAGCAAC GATTATTGAT GCTGAACATG TTAAGAAGTC AGATAAGCTT    1740
76  TTAAAAATTC AAGTAGACTT AGATTCTGAA CAAAGACAAA TTGTATCAGG AATTGCCAAA    1800
77  TTCTATACAC CAGATGATAT TATTGGTAAA AAAGTAGCAG TTGTTACTAA CCTGAAACCA    1860
78  GCTAAATTAA TGGGACAAAA ATCTGAAGGT ATGATATTAT CTGCTGAAAA AGATGGTGTA    1920
79  TTAACCTTAG TAAGTTTACC AAGTGCAATT CCAATGGTG CAGTGATTAA ATAA          1974

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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93  Met Ala Lys Glu Thr Phe Tyr Ile Thr Thr Pro Ile Tyr Tyr Pro Ser
94      1             5             10             15
95  Gly Asn Leu His Ile Gly His Ala Tyr Ser Thr Val Ala Gly Asp Val
96             20             25             30
97  Ile Ala Arg Tyr Lys Arg Met Gln Gly Tyr Asp Val Arg Tyr Leu Thr
98             35             40             45
99  Gly Thr Asp Glu His Gly Gln Lys Ile Gln Glu Lys Ala Gln Lys Ala

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RAW SEQUENCE LISTING PATENT APPLICATION US/08/785,455

 DATE: 02/21/97
 TIME: 15:30:07

INPUT SET: S15668.raw

100	50	55	60														
101	Gly	Lys	Thr	Glu	Ile	Glu	Tyr	Leu	Asp	Glu	Met	Ile	Ala	Gly	Ile	Lys	
102	65					70				75					80		
103	Gln	Leu	Trp	Ala	Lys	Leu	Glu	Ile	Ser	Asn	Asp	Asp	Phe	Ile	Arg	Thr	
104					85					90					95		
105	Thr	Glu	Glu	Arg	His	Lys	His	Val	Val	Glu	Gln	Val	Phe	Glu	Arg	Leu	
106				100					105					110			
107	Leu	Lys	Gln	Gly	Asp	Ile	Tyr	Leu	Gly	Glu	Tyr	Glu	Gly	Trp	Tyr	Ser	
108			115					120					125				
109	Val	Pro	Asp	Glu	Thr	Tyr	Tyr	Thr	Glu	Ser	Gln	Leu	Val	Asp	Pro	Gln	
110		130					135					140					
111	Tyr	Glu	Asn	Gly	Lys	Ile	Ile	Gly	Gly	Lys	Ser	Pro	Asp	Ser	Gly	His	
112	145					150				155					160		
113	Glu	Val	Glu	Leu	Val	Lys	Glu	Glu	Ser	Tyr	Phe	Phe	Asn	Ile	Ser	Lys	
114					165					170					175		
115	Tyr	Thr	Asp	Arg	Leu	Leu	Glu	Phe	Tyr	Asp	Gln	Asn	Pro	Asp	Phe	Ile	
116			180					185					190				
117	Gln	Pro	Pro	Ser	Arg	Lys	Asn	Glu	Met	Ile	Asn	Asn	Phe	Ile	Lys	Pro	
118		195					200					205					
119	Gly	Leu	Ala	Asp	Leu	Ala	Val	Ser	Arg	Thr	Ser	Phe	Asn	Trp	Gly	Val	
120		210					215					220					
121	His	Val	Pro	Ser	Asn	Pro	Lys	His	Val	Val	Tyr	Val	Trp	Ile	Asp	Ala	
122	225					230				235					240		
123	Leu	Val	Asn	Tyr	Ile	Ser	Ala	Leu	Gly	Tyr	Leu	Ser	Asp	Asp	Glu	Ser	
124					245					250					255		
125	Leu	Phe	Asn	Lys	Tyr	Trp	Pro	Ala	Asp	Ile	His	Leu	Met	Ala	Lys	Glu	
126			260					265					270				
127	Ile	Val	Arg	Phe	His	Ser	Ile	Ile	Trp	Pro	Ile	Leu	Leu	Met	Ala	Leu	
128		275					280					285					
129	Asp	Leu	Pro	Leu	Pro	Lys	Lys	Val	Phe	Ala	His	Gly	Trp	Ile	Leu	Met	
130		290					295					300					
131	Lys	Asp	Gly	Lys	Met	Ser	Lys	Ser	Lys	Gly	Asn	Val	Val	Asp	Pro	Asn	
132	305					310				315					320		
133	Ile	Leu	Ile	Asp	Arg	Tyr	Gly	Leu	Asp	Ala	Thr	Arg	Tyr	Tyr	Leu	Met	
134					325					330					335		
135	Arg	Glu	Leu	Pro	Phe	Gly	Ser	Asp	Gly	Val	Phe	Thr	Pro	Glu	Ala	Phe	
136			340					345					350				
137	Val	Glu	Arg	Thr	Asn	Phe	Asp	Leu	Ala	Asn	Asp	Leu	Gly	Asn	Leu	Val	
138		355					360					365					
139	Asn	Arg	Thr	Ile	Ser	Met	Val	Asn	Lys	Tyr	Phe	Asp	Gly	Glu	Leu	Pro	
140		370					375					380					
141	Ala	Tyr	Gln	Gly	Pro	Leu	His	Glu	Leu	Asp	Glu	Glu	Met	Glu	Ala	Met	
142	385					390				395					400		
143	Ala	Leu	Glu	Thr	Val	Lys	Ser	Tyr	Thr	Glu	Ser	Met	Glu	Ser	Leu	Gln	
144					405					410					415		
145	Phe	Ser	Val	Ala	Leu	Ser	Thr	Val	Trp	Lys	Phe	Ile	Ser	Arg	Thr	Asn	
146			420					425					430				
147	Lys	Tyr	Ile	Asp	Glu	Thr	Thr	Pro	Trp	Val	Leu	Ala	Lys	Asp	Asp	Ser	
148		435					440					445					
149	Gln	Lys	Asp	Met	Leu	Gly	Asn	Val	Met	Ala	His	Leu	Val	Glu	Asn	Ile	
150		450					455					460					
151	Arg	Tyr	Ala	Ala	Val	Leu	Leu	Arg	Pro	Phe	Leu	Thr	His	Ala	Pro	Lys	
152	465					470				475					480		

DATE: 02/21/97
TIME: 15:30:11

153	Glu Ile Phe Glu Gln Leu Asn Ile Asn Asn Pro Gln Ph Met Glu Phe
154	485 490 495
155	Ser Ser Leu Glu Gln Tyr Gly Val Leu Thr Glu Ser Ile Met Val Thr
156	500 505 510
157	Gly Gln Pro Lys Pro Ile Phe Pro Arg Leu Asp Ser Glu Ala Glu Ile
158	515 520 525
159	Ala Tyr Ile Lys Glu Ser Met Gln Pro Pro Ala Thr Glu Glu Glu Lys
160	530 535 540
161	Glu Glu Ile Pro Ser Lys Pro Gln Ile Asp Ile Lys Asp Phe Asp Lys
162	545 550 555
163	Val Glu Ile Lys Ala Ala Thr Ile Ile Asp Ala Glu His Val Lys Lys
164	565 570 575
165	Ser Asp Lys Leu Leu Lys Ile Gln Val Asp Leu Asp Ser Glu Gln Arg
166	580 585 590
167	Gln Ile Val Ser Gly Ile Ala Lys Phe Tyr Thr Pro Asp Asp Ile Ile
168	595 600 605
169	Gly Lys Lys Val Ala Val Val Thr Asn Leu Lys Pro Ala Lys Leu Met
170	610 615 620
171	Gly Gln Lys Ser Glu Gly Met Ile Leu Ser Ala Glu Lys Asp Gly Val
172	625 630 635
173	Leu Thr Leu Val Ser Leu Pro Ser Ala Ile Pro Asn Gly Ala Val Ile
174	645 650 655
175	Lys
176	
177	